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RAW SEQUENCE LISTING

DATE: 06/27/2003

PATENT APPLICATION: US/09/802,285A

TIME: 12:51:58

Input Set : A:\M00656.70063.US Sequence Listing.txt

Output Set: N:\CRF4\06272003\I802285A.raw

```

4 <110> APPLICANT: Liu, Dongfang
5      Pojasek, Kevin
6      Shriver, Zachary
7      Holley, Kristine
8      El-Shabrawi, Yosuf
9      Venkataraman, Ganesh
10     Sasisekharan, Ram
12 <120> TITLE OF INVENTION: Heparinase III and Uses Thereof
14 <130> FILE REFERENCE: M00656.70063.US
C--> 16 <140> CURRENT APPLICATION NUMBER: US/09/802,285A
C--> 17 <141> CURRENT FILING DATE: 2001-03-08
19 <150> PRIOR APPLICATION NUMBER: US 09/802,285
20 <151> PRIOR FILING DATE: 2001-03-08
22 <160> NUMBER OF SEQ ID NOS: 3
24 <170> SOFTWARE: PatentIn version 3.0
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 1980
28 <212> TYPE: DNA
29 <213> ORGANISM: Pedobacter heparinus
31 <400> SEQUENCE: 1
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36 tattccggac tggaaaaggt taataaagca gttgctgccc gcaactatga cgatgcccgc      180
38 aaagcattac tggcatacta cagggaaaaa agtaaggcca gggaacctga ttccagtaat      240
40 gcagaaaaagc ctgccgatat acgccagccc atagataagg ttacgcgtga aatggccgac      300
42 aaggctttgg tccaccagtt tcaaccgcac aaaggctacg gctattttga ttatggtaaa      360
44 gacatcaact ggcagatgtg gccggtaaaa gacaatgaag tacgctggca gttgcaccgt      420
46 gtaaaatggt ggcaggctat ggccctgggt tatcacgcta cgggcgatga aaaatatgca      480
48 agagaatggg tatatcagta cagcgattgg gccagaaaaa acccattggg cctgtcgcag      540
50 gataatgata aatttgtgtg gcggcccctt gaagtgtcgg acagggtaca agtcttccc      600
52 ccaaccttca gcttatttgt aaactcgcca gcctttaccc cagccttttt aatggaattt      660
54 ttaaacagtt accaccaaca ggccgattat ttatctacgc attatgccga acagggaaac      720
56 caccgtttat ttgaagccca acgcaacttg tttgcagggg tatctttccc tgaatttaaa      780
58 gattcaccaa gatggaggca aaccggcata tcggtgctga acaccgagat caaaaaacag      840
60 gtttatgccg atgggatgca gtttgaactt tcaccaattt accatgtagc tgccatcgat      900
62 atcttcttaa aggcctatgg ttctgcaaaa cgagttaacc ttgaaaaaga atttccgcaa      960
64 tcttatgtac aaactgtaga aaatatgatt atggcgctga tcagtatttc actgccagat      1020
66 tataacaccc ctatgtttgg agattcatgg attacagata aaaatttcag gatggcacag      1080
68 tttgccagct gggcccgggt tttcccggca aaccaggcca taaaatat ttgctacagat      1140
70 ggcaaacaag gtaaggcgcc taacttttta tccaaagcat tgagcaatgc aggcttttat      1200
72 acgttttaga gcggatggga taaaaatgca accgttatgg tattaaaagc cagtcctccc      1260
74 ggggaatttc atgccagccg ggataacggg acttttgaac tttttataaa gggcagaaac      1320
76 ttacccccag acgcccgggt atttgtgtat agcggcgacg aagccatcat gaaactgcgg      1380

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78 aactggtacc gtcaaaccgc catacacagc acgcttacac tcgacaatca aaatatggtc 1440
80 attaccaaaag cccggcaaaa caaatgggaa acaggaaata accttgatgt gcttacctat 1500
82 accaacccaa gctatccgaa tctggaccat cagcgcatgt tacttttcat caacaaaaaa 1560
84 tacttttctgg tcatcgatag ggcaataggc gaagctaccg gaaacctggg cgtacactgg 1620
86 cagcttaaag aagacagcaa ccctgttttc gataagacaa agaaccgggt ttacaccact 1680
88 tacagagatg gtaacaacct gatgatccaa tcgttgaatg cggacaggac cagcctcaat 1740
90 gaagaagaag gaaaggtatc ttatgtttac aataaggagc tgaaaagacc tgctttcgt 1800
92 ttgaaaagc ctaaaaagaa tgccggcaca caaaattttg tcagtatagt ttatccatac 1860
94 gacggccaga aggtccaga gatcagcata cgggaaaaca agggcaatga ttttgagaaa 1920
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99 <211> LENGTH: 659
100 <212> TYPE: PRT
101 <213> ORGANISM: Pedobacter heparinus
103 <400> SEQUENCE: 2
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106 1 5 10 15
108 Leu Ser Ser Gly Asn Ile Leu Ala Gln Ser Ser Ser Ile Thr Arg Lys
109 20 25 30
111 Asp Phe Asp His Ile Asn Leu Glu Tyr Ser Gly Leu Glu Lys Val Asn
112 35 40 45
114 Lys Ala Val Ala Ala Gly Asn Tyr Asp Asp Ala Ala Lys Ala Leu Leu
115 50 55 60
117 Ala Tyr Tyr Arg Glu Lys Ser Lys Ala Arg Glu Pro Asp Phe Ser Asn
118 65 70 75 80
121 Ala Glu Lys Pro Ala Asp Ile Arg Gln Pro Ile Asp Lys Val Thr Arg
122 85 90 95
124 Glu Met Ala Asp Lys Ala Leu Val His Gln Phe Gln Pro His Lys Gly
125 100 105 110
127 Tyr Gly Tyr Phe Asp Tyr Gly Lys Asp Ile Asn Trp Gln Met Trp Pro
128 115 120 125
130 Val Lys Asp Asn Glu Val Arg Trp Gln Leu His Arg Val Lys Trp Trp
131 130 135 140
133 Gln Ala Met Ala Leu Val Tyr His Ala Thr Gly Asp Glu Lys Tyr Ala
134 145 150 155 160
136 Arg Glu Trp Val Tyr Gln Tyr Ser Asp Trp Ala Arg Lys Asn Pro Leu
137 165 170 175
139 Gly Leu Ser Gln Asp Asn Asp Lys Phe Val Trp Arg Pro Leu Glu Val
140 180 185 190
142 Ser Asp Arg Val Gln Ser Leu Pro Pro Thr Phe Ser Leu Phe Val Asn
143 195 200 205
145 Ser Pro Ala Phe Thr Pro Ala Phe Leu Met Glu Phe Leu Asn Ser Tyr
146 210 215 220
148 His Gln Gln Ala Asp Tyr Leu Ser Thr His Tyr Ala Glu Gln Gly Asn
149 225 230 235 240
151 His Arg Leu Phe Glu Ala Gln Arg Asn Leu Phe Ala Gly Val Ser Phe
152 245 250 255
154 Pro Glu Phe Lys Asp Ser Pro Arg Trp Arg Gln Thr Gly Ile Ser Val
155 260 265 270

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157 Leu Asn Thr Glu Ile Lys Lys Gln Val Tyr Ala Asp Gly Met Gln Phe
158      275      280      285
160 Glu Leu Ser Pro Ile Tyr His Val Ala Ala Ile Asp Ile Phe Leu Lys
161      290      295      300
163 Ala Tyr Gly Ser Ala Lys Arg Val Asn Leu Glu Lys Glu Phe Pro Gln
164 305      310      315      320
166 Ser Tyr Val Gln Thr Val Glu Asn Met Ile Met Ala Leu Ile Ser Ile
167      325      330      335
169 Ser Leu Pro Asp Tyr Asn Thr Pro Met Phe Gly Asp Ser Trp Ile Thr
170      340      345      350
172 Asp Lys Asn Phe Arg Met Ala Gln Phe Ala Ser Trp Ala Arg Val Phe
173      355      360      365
175 Pro Ala Asn Gln Ala Ile Lys Tyr Phe Ala Thr Asp Gly Lys Gln Gly
176      370      375      380
178 Lys Ala Pro Asn Phe Leu Ser Lys Ala Leu Ser Asn Ala Gly Phe Tyr
179 385      390      395      400
182 Thr Phe Arg Ser Gly Trp Asp Lys Asn Ala Thr Val Met Val Leu Lys
183      405      410      415
185 Ala Ser Pro Pro Gly Glu Phe His Ala Gln Pro Asp Asn Gly Thr Phe
186      420      425      430
188 Glu Leu Phe Ile Lys Gly Arg Asn Phe Thr Pro Asp Ala Gly Val Phe
189      435      440      445
191 Val Tyr Ser Gly Asp Glu Ala Ile Met Lys Leu Arg Asn Trp Tyr Arg
192      450      455      460
194 Gln Thr Arg Ile His Ser Thr Leu Thr Leu Asp Asn Gln Asn Met Val
195 465      470      475      480
197 Ile Thr Lys Ala Arg Gln Asn Lys Trp Glu Thr Gly Asn Asn Leu Asp
198      485      490      495
200 Val Leu Thr Tyr Thr Asn Pro Ser Tyr Pro Asn Leu Asp His Gln Arg
201      500      505      510
203 Ser Val Leu Phe Ile Asn Lys Lys Tyr Phe Leu Val Ile Asp Arg Ala
204      515      520      525
206 Ile Gly Glu Ala Thr Gly Asn Leu Gly Val His Trp Gln Leu Lys Glu
207      530      535      540
209 Asp Ser Asn Pro Val Phe Asp Lys Thr Lys Asn Arg Val Tyr Thr Thr
210 545      550      555      560
212 Tyr Arg Asp Gly Asn Asn Leu Met Ile Gln Ser Leu Asn Ala Asp Arg
213      565      570      575
215 Thr Ser Leu Asn Glu Glu Glu Gly Lys Val Ser Tyr Val Tyr Asn Lys
216      580      585      590
218 Glu Leu Lys Arg Pro Ala Phe Val Phe Glu Lys Pro Lys Lys Asn Ala
219      595      600      605
221 Gly Thr Gln Asn Phe Val Ser Ile Val Tyr Pro Tyr Asp Gly Gln Lys
222      610      615      620
224 Ala Pro Glu Ile Ser Ile Arg Glu Asn Lys Gly Asn Asp Phe Glu Lys
225 625      630      635      640
227 Gly Lys Leu Asn Leu Thr Leu Thr Ile Asn Gly Lys Gln Gln Leu Val
228      645      650      655
230 Leu Val Pro

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233 <210> SEQ ID NO: 3  
234 <211> LENGTH: 25  
235 <212> TYPE: PRT  
236 <213> ORGANISM: Flavobacterium heparinum  
238 <400> SEQUENCE: 3  
241 Gln Val Tyr Ala Asp Gly Met Gln Phe Glu Leu Ser Pro Ile Tyr His  
242 1 5 10 15  
244 Val Ala Ala Ile Asp Ile Phe Leu Lys  
245 20 25

VERIFICATION SUMMARY

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L:16 M:270 C: Current Application Number differs, Replaced Current Application Number

L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date